



## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

## SEQUENCE LISTING

<110> Hoff, Glenn  
Schmollinger, Jan  
Hodi, F. Stephen  
Mollick, Joseph

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<130> 2486/109

<140> US 09/762,577

<141> 2002-08-29

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<151> 1998-08-07

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35      40      45
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50      55      60
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65      70      75      80
Gln Gly Thr Ser Arg Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala
85      90      95
Gln Gln Asp Leu Gln Gly Thr Ser Gln Pro Arg Pro His Arg Arg Pro
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Gln Ala Pro Ala Arg Gln Asp Leu Gln Gly Met Ser Gln Pro Arg Ala
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Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala Arg Gln Asp Leu
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 Val Leu Gln Ala Leu Tyr Phe Cys Arg Pro Phe Arg Glu Asn Val Leu  
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 65 70 75 80  
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 210 215 220  
 Gln Lys Tyr Tyr Cys Glu Thr Cys Cys Ser Lys Gln Glu Ala Gln Lys  
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 Arg Met Arg Val Lys Lys Leu Pro Met Ile Leu Ala Leu His Leu Lys  
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 Arg Phe Lys Tyr Met Glu Gln Leu His Arg Tyr Thr Lys Leu Ser Tyr  
 260 265 270  
 Arg Val Val Phe Pro Leu Glu Leu Arg Leu Phe Asn Thr Ser Ser Asp  
 275 280 285  
 Ala Val Asn Leu Asp Arg Met Tyr Asp Leu Val Ala Val Val Val His  
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 305 310 315 320  
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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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 <212> DNA  
 <213> homo sapiens

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 <212> PRT  
 <213> homo sapiens

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			20					25					30		
Pro	Asn	Leu	Ser	Phe	Tyr	Arg	Asn	Glu	Ile	Arg	Phe	Leu	Pro	Asn	Gly
			35				40					45			
Cys	Phe	Ile	Glu	Asp	Ile	Leu	Gln	Asn	Trp	Thr	Asp	Asn	Tyr	Asp	Leu
	50					55				60					
Leu	Glu	Asp	Asn	His	Ser	Tyr	Ile	Gln	Trp	Leu	Phe	Pro	Leu	Arg	Glu
65					70				75					80	
Pro	Gly	Val	Asn	Trp	His	Ala	Lys	Pro	Leu	Thr	Leu	Arg	Glu	Val	Glu
			85					90					95		
Val	Phe	Lys	Ser	Ser	Gln	Glu	Ile	Gln	Glu	Arg	Leu	Val	Arg	Ala	Tyr
			100					105					110		



2486-109REPLACEMENTSEQLISTCOPY2.TXT

Glu Leu Met Leu Gly Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr  
 115 120 125  
 Gly Thr Val Gly Arg Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu  
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 Asn Trp Arg Ser His Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser  
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 Leu Gly Glu Leu Gly Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe  
 165 170 175  
 Phe Leu Glu Glu Thr Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln  
 180 185 190  
 Ser Ala Leu Asp Tyr Phe Met Phe Ala Val Arg Cys Arg His Gln Arg  
 195 200 205  
 Arg Gln Leu Val His Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys  
 210 215 220  
 Phe Val Trp Gly Pro Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser  
 225 230 235 240  
 Leu Pro His Pro Leu Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser  
 245 250 255  
 Pro Gly Asp Pro Asp His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly  
 260 265 270  
 Pro Glu His Ser Lys Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro  
 275 280 285  
 Arg Ser Val Glu Pro Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly  
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 Asp Glu Ala Gly Gly His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro  
 305 310 315 320  
 Lys Glu Ser Lys Lys Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro  
 325 330 335  
 Pro Thr Glu Pro Gly Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala  
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 355 360 365  
 Thr Gln Glu Val Gly Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys  
 370 375 380  
 Arg Gln Pro Leu Gly Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg  
 385 390 395 400  
 Lys Val Asp Glu Gly Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly  
 405 410 415  
 Ala Gln Thr Leu Ala Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro  
 420 425 430  
 Lys Ala Gly His Ser Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg  
 435 440 445  
 Thr Gly Pro Lys Glu Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly  
 450 455 460  
 Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser  
 465 470 475 480  
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 485 490 495  
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 Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala  
 515 520 525  
 Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly  
 530 535 540  
 Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys Ala Gly Glu  
 545 550 555 560  
 Ala Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala Lys Ser Gly  
 565 570 575  
 Lys Pro

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

<211> 176  
 <212> PRT  
 <213> homo sapiens

<400> 19  
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 Asp Thr Val Arg Thr Gly Leu Arg Arg Thr Gln Lys Val Glu Arg Gly  
 35 40 45  
 Pro Lys Lys Val Pro Leu Gly Ala His Arg Arg Pro Gln Ala Pro Ala  
 50 55 60  
 Gln Gln Asp Leu Gln Gly Thr Ser Gln Pro Arg Ala His Arg Arg Pro  
 65 70 75 80  
 Gln Ala Pro Ala Arg Gln Asp Leu Gln Gly Met Ser Gln Pro Arg Ala  
 85 90 95  
 His Arg Arg Pro Gln Ala Pro Ala Arg Gln Asp Leu Gln Gly Thr Ser  
 100 105 110  
 Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala Arg Gln Asp Leu  
 115 120 125  
 Gln Gly Thr Ser Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala  
 130 135 140  
 Arg Gln Asp Leu Gln Gly Met Ser Gln Pro Arg Arg Gly Arg Gln Gln  
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<210> 20  
 <211> 49  
 <212> PRT  
 <213> homo sapiens

<400> 20  
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<210> 21  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 21  
 Ala His Arg Arg Pro Gln Ala Pro Ala Gln Gln Asp Leu Gln Gly Thr  
 1 5 10 15  
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 Leu Gln Gly Thr Ser Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro  
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 Ala Gln  
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<210> 22  
 <211> 9

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 22

Ser Leu Gly Ser Pro Val Leu Gly Leu  
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&lt;210&gt; 23

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 23

Arg Leu Ala Ser Phe Tyr Asp Trp Pro Leu  
1 5 10

&lt;210&gt; 24

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (2)...(17)

<223> Xaa at 2 is Thr or Met;  
Xaa at 4 is Gln or Arg;  
Xaa at 7 is Ala or Pro;  
Xaa at 16 is Arg or Gln.

&lt;221&gt; VARIANT

&lt;222&gt; 2, 4, 7, 16

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 24

Gly Xaa Ser Xaa Pro Arg Xaa His Arg Arg Pro Gln Ala Pro Ala Xaa  
1 5 10 15  
Gln Asp Leu Gln  
20

&lt;210&gt; 25

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 25

Ala His Arg Arg Pro Gln Ala Pro Ala Gln Gln Asp Leu Gln  
1 5 10

&lt;210&gt; 26

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 26

Gly Thr Ser Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala Arg  
1 5 10 15  
Gln Asp Leu Gln  
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2486-109REPLACEMENTSEQLISTCOPY2.TXT

<210> 27  
 <211> 20  
 <212> PRT  
 <213> homo sapiens

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 1 5 10 15  
 Gln Asp Leu Gln  
 20

<210> 28  
 <211> 20  
 <212> PRT  
 <213> homo sapiens

<400> 28  
 Gly Thr Ser Gln Pro Arg Ala His Arg Arg Pro Gln Ala Pro Ala Gln  
 1 5 10 15  
 Gln Asp Leu Gln  
 20

<210> 29  
 <211> 20  
 <212> PRT  
 <213> homo sapiens

<400> 29  
 Gly Thr Ser Gln Pro Arg Pro His Arg Arg Pro Gln Ala Pro Ala Arg  
 1 5 10 15  
 Gln Asp Leu Gln  
 20

<210> 30  
 <211> 20  
 <212> PRT  
 <213> homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(20)  
 <223> Xaa at 9 is Arg or Ser;  
 Xaa at 14 is Ala or Thr;  
 Xaa at 15 is Gly or Arg;  
 Xaa at 20 is Glu or Lys

<221> VARIANT  
 <222> 9, 14, 15, 20  
 <223> Xaa = Any Amino Acid

<400> 30  
 Ser Pro Ser Glu Thr Pro Gly Pro Xaa Pro Ala Gly Pro Xaa Xaa Asp  
 1 5 10 15  
 Glu Pro Ala Xaa  
 20

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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 <211> 20  
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 <213> homo sapiens

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<210> 32  
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 <212> PRT  
 <213> homo sapiens

<400> 32  
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 Glu Pro Ala Glu  
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<210> 33  
 <211> 20  
 <212> PRT  
 <213> homo sapiens

<400> 33  
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 Glu Pro Ala Lys  
                   20

<210> 34  
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 <212> DNA  
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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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 <211> 618  
 <212> PRT  
 <213> homo sapiens

<400> 35  
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 Arg His Asn Tyr Pro Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr  
 20 25 30  
 Pro Asn Leu Ser Phe Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly  
 35 40 45  
 Cys Phe Ile Glu Asp Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu  
 50 55 60  
 Leu Glu Asp Asn His Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu  
 65 70 75 80  
 Pro Gly Val Asn Trp His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu  
 85 90 95  
 Val Phe Lys Ser Ser Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr  
 100 105 110  
 Ala Ala His Ala Gly Leu Leu Arg Asp Pro Ala Gly Gly Pro Arg His  
 115 120 125  
 Gly His Gly Gly Pro Ser Thr Glu Leu Pro Glu Ala Leu Pro Glu Pro  
 130 135 140  
 Glu Leu Arg Ser His Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser  
 145 150 155 160  
 Leu Gly Glu Leu Gly Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe  
 165 170 175  
 Phe Leu Glu Glu Ser Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln  
 180 185 190  
 Ser Ala Leu Asp Tyr Phe Met Phe Ala Val Gly Cys Arg His Gln Arg

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

Arg	Gln	195	Leu	Val	His	Phe	Ala	200	Trp	Glu	His	Phe	Arg	205	Pro	Arg	Cys	Lys
210	Phe	Val	Trp	Gly	Pro	Gln	215	Asp	Lys	Leu	Arg	Arg	220	Phe	Lys	Pro	Ser	Ser
225	Leu	Pro	His	Pro	Leu	230	Glu	Gly	Ser	Arg	Lys	Val	235	Glu	Glu	Glu	Gly	Ser
	Pro	Gly	Asp	Pro	245	Asp	His	Glu	Ala	Ser	250	Thr	Gln	Gly	Arg	Thr	Cys	Gly
	Pro	Glu	His	Ser	260	Lys	Gly	Gly	Gly	Arg	265	Val	Asp	Glu	Gly	Pro	Gln	Pro
	Arg	Ser	Val	Glu	Pro	Gln	280	Asp	Ala	Gly	Pro	Leu	285	Glu	Arg	Ser	Gln	Gly
	290	Asp	Glu	Ala	Gly	Gly	His	295	Gly	Glu	Asp	Arg	300	Pro	Glu	Pro	Leu	Ser
	305	Lys	Glu	Ser	Lys	Lys	Arg	Lys	Leu	Glu	Leu	Ser	315	Arg	Arg	Glu	Gln	Pro
	Pro	Thr	Glu	Pro	325	Gly	Pro	Gln	Ser	Ala	Ser	Glu	330	Val	Glu	Lys	Ile	Ala
	Leu	Asn	Leu	Glu	340	Gly	Cys	Ala	Leu	Ser	Gln	Gly	345	Ser	Leu	Arg	Thr	Gly
	355	Thr	Gln	Glu	Val	Gly	Gly	Gln	Asp	Pro	Gly	Glu	360	Ala	Val	Gln	Pro	Cys
	370	Arg	Gln	Pro	Leu	Gly	Ala	Arg	Val	Ala	Asp	Lys	380	Val	Arg	Lys	Arg	Arg
	385	Lys	Val	Asp	Glu	Gly	Ala	Gly	Asp	Ser	Ala	Ala	395	Val	Ala	Ser	Gly	Gly
		Ala	Gln	Thr	Leu	Ala	Leu	Ala	Gly	Ser	Pro	Ala	410	Pro	Ser	Gly	His	Pro
		Lys	Ala	Gly	His	Ser	Glu	Asn	Gly	Val	Glu	Glu	425	Asp	Thr	Glu	Gly	Arg
		Thr	Gly	Pro	Lys	Glu	Gly	Thr	Pro	Gly	Ser	Pro	440	Ser	Glu	Thr	Pro	Gly
		Pro	Ser	Pro	Ala	Gly	Pro	Ala	Gly	Asp	Glu	Pro	455	Pro	Ala	Glu	Ser	Pro
		465	Glu	Thr	Pro	Gly	Pro	Arg	Pro	Ala	Gly	Pro	470	Ala	Gly	Asp	Glu	Pro
		Glu	Ser	Pro	Ser	Glu	Thr	Pro	Gly	Pro	Arg	Pro	485	Pro	Ala	Gly	Pro	Ala
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		Pro	Arg	Pro	Ala	Gly	Pro	Ala	Gly	Asp	Glu	Pro	530	Ala	Glu	Ser	Pro	Ser
		545	Glu	Thr	Pro	Gly	Pro	Arg	Pro	Ala	Gly	Pro	550	Ala	Gly	Asp	Glu	Pro
		Glu	Ser	Pro	Ser	Glu	Thr	Pro	Gly	Pro	Ser	Pro	565	Ala	Gly	Pro	Thr	Arg
		Asp	Glu	Pro	Ala	Lys	Ala	Gly	Glu	Ala	Ala	Glu	580	Leu	Gln	Asp	Ala	Glu
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		610						615										

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 <212> DNA  
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 cctgcccgcc gccccccact ccagaagggt caatttacaa agacaggggc gcaggggaga 120



## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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gctgggtggg gaagacacag ccaggccagg aggccttctgc aggccttggc tatccctgag 180
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tgggtcacgg gtcacgaagc agagcctgag gggagcccgc agcagctccg gagccccagg 300
ccctgcagca gggacaggag gaccaagacg ccgacggcac tcctttcctt aaggc 355

```

```

<210> 37
<211> 270
<212> DNA
<213> homo sapiens

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<400> 37
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tatagtggcc ccacaggagg cagcactgtg ggtcatgggt cacgggtcac gaagcagagc 180
ctgagggggag cccgcagcag ctccggagcc ccagccctgc agcagggaca ggaggaccaa 240
gacgccgacg ggactccttt ccttaaggct 270

```

```

<210> 38
<211> 141
<212> DNA
<213> homo sapiens

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```

<400> 38
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ctgcccgcgg cccccactc cagaagggtc aatttataaa gacaggggag caggggagag 120
ctgggtgggg aagacacagc c 141

```

```

<210> 39
<211> 192
<212> DNA
<213> homo sapiens

```

```

<400> 39
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ctggggctcc ggagctgctg cgggctccct caggctctgc ttcgtgacct gtgacctatg 180
accacagtg ct 192

```

```

<210> 40
<211> 309
<212> DNA
<213> homo sapiens

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```

<220>
<221> misc_feature
<222> 1, 80, 254, 265, 275, 282, 290, 304
<223> n = A,T,C or G

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<400> 40
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ggangggccc 309

```

```

<210> 41
<211> 178
<212> DNA
<213> homo sapiens

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<400> 41
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```

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

tcccctgcg cccctgtcttt gtaaattgac ctttctggag tggggggcgg cgggcagggc 120  
 tgcttttctt agtctgatac caagcaaggc cttttctgaa taaattcatt tgactttg 178

<210> 42  
 <211> 166  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> 15, 22, 24, 76, 77, 119, 153, 163  
 <223> n = A,T,C or G

<400> 42  
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 cctttttttt taaatnnacc cttctggagt ggggggcggc gggcagggct gctttttttna 120  
 gtctgatgcc aagcaaggcc ttttttgaat aanttcattt ganttt 166

<210> 43  
 <211> 209  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> 11, 90, 138, 166, 185, 190, 200  
 <223> n = A,T,C or G

<400> 43  
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 ttgaggagga cacagaangt caaacggggc ccaaagaagg taccntggg gagcccatca 180  
 gaganccan gcccagccn ggcaggac 209

<210> 44  
 <211> 241  
 <212> DNA  
 <213> homo sapiens

<400> 44  
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 acaaagacag gggcgcttg gagagctggg tggggaagac acagccaggc caggaggctt 180  
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 a 241

<210> 45  
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 <213> homo sapiens

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2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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	Lys	Asn	Arg	Thr	Met	340	Leu	Phe	Gln	Val	Gly	345	Arg	Phe	Glu	Ile	Asn	350	Leu
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	Ile	Ser	Ser	Cys	Ser	370	Gln	Gly	Ile	Lys	His	375	Val	Asp	His	Phe	Gly	380	Phe
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	Leu	Lys	Gln	Ala	Phe	420	Ser	Thr	Ala	Ala	Leu	425	Ala	Gln	Ser	Ala	Lys	430	Thr
	Gln	Ile	Lys	Leu	Cys	435	Glu	Ala	Cys	Pro	Met	440	His	Ser	Leu	His	Lys	445	Leu
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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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Pro	Asp	Glu	Leu	Lys	Thr	Thr	Val	Glu	Glu	Arg	Lys	Ser	Ser	Glu	Ala
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Arg	Ala	Glu	Val	Leu	Lys	Ser	Glu	Asp	Gly	Ala	Ser	Leu	Pro	Val	Met
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Asp	Leu	Thr	Glu	Leu	Pro	Lys	Cys	Thr	Val	Cys	Leu	Glu	Arg	Met	Asp
			260					265					270		
Glu	Ser	Val	Asn	Gly	Ile	Leu	Thr	Thr	Leu	Cys	Asn	His	Ser	Phe	His
		275					280					285			
Ser	Gln	Cys	Leu	Gln	Arg	Trp	Asp	Asp	Thr	Thr	Cys	Pro	Val	Cys	Arg
	290					295					300				
Tyr	Cys	Gln	Thr	Pro	Glu	Pro	Val	Glu	Glu	Asn	Lys	Cys	Phe	Glu	Cys
305					310					315					320
Gly	Val	Gln	Glu	Asn	Leu	Trp	Ile	Cys	Leu	Ile	Cys	Gly	His	Ile	Gly
				325					330					335	
Cys	Gly	Arg	Tyr	Val	Ser	Arg	His	Ala	Tyr	Lys	His	Phe	Glu	Glu	Thr
			340					345					350		
Gln	His	Thr	Tyr	Ala	Met	Gln	Leu	Thr	Asn	His	Arg	Val	Trp	Asp	Tyr
		355					360					365			
Ala	Gly	Asp	Asn	Tyr	Val	His	Arg	Leu	Val	Ala	Ser	Lys	Thr	Asp	Gly
	370					375					380				
Lys	Ile	Val	Gln	Tyr	Glu	Cys	Glu	Gly	Asp	Thr	Cys	Gln	Glu	Glu	Lys
385					390					395					400
Ile	Asp	Ala	Leu	Gln	Leu	Glu	Tyr	Ser	Tyr	Leu	Leu	Thr	Ser	Gln	Leu
				405					410					415	
Glu	Ser	Gln	Arg	Ile	Tyr	Trp	Glu	Asn	Lys	Ile	Val	Arg	Ile	Glu	Lys
			420					425					430		
Asp	Thr	Ala	Glu	Glu	Ile	Asn	Asn	Met	Lys	Thr	Lys	Phe	Lys	Glu	Thr
		435					440					445			
Ile	Glu	Lys	Cys	Asp	Asn	Leu	Glu	His	Lys	Leu	Asn	Asp	Leu	Leu	Lys
	450					455					460				
Glu	Lys	Gln	Ser	Val	Glu	Arg	Lys	Cys	Thr	Gln	Leu	Asn	Thr	Lys	Val
465					470					475					480
Ala	Lys	Leu	Thr	Asn	Glu	Leu	Lys	Glu	Glu	Gln	Glu	Met	Asn	Lys	Cys
				485					490					495	
Leu	Arg	Ala	Asn	Gln	Val	Leu	Leu	Gln	Asn	Lys	Leu	Lys	Glu	Glu	Glu
			500					505					510		
Arg	Val	Leu	Lys	Glu	Thr	Cys	Asp	Gln	Lys	Asp	Leu	Gln	Ile	Thr	Glu
		515					520					525			
Ile	Gln	Glu	Gln	Leu	Arg	Asp	Val	Met	Phe	Tyr	Leu	Glu	Thr	Gln	Gln
	530					535					540				



## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

Lys Ile Asn His Leu Pro Ala Glu Thr Arg Gln Lys Ser Arg Arg Asp  
 545 550 555 560  
 Arg Ser Thr Ser Pro Trp Pro Arg Pro Arg Ala Leu Pro Leu Arg Gly  
 565 570 575  
 Ala Val Gly Ser Cys Pro Pro Gly Arg Ala Ala Arg Gly Ala Ser  
 580 585 590  
 Asp Leu Gln Ser Asn Arg His Pro  
 595 600

<210> 49  
 <211> 226  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> 163, 168  
 <223> n = A,T,C or G

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 ccatcagccc ccatttctgc tgcaaacctg gtcagagcca gtnttcntc catgggacct 180  
 aaagacagt ccaagtgcct gcaccgtgga ccacagccga gccact 226

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 <211> 441  
 <212> DNA  
 <213> homo sapiens

<400> 50  
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 tttctgtgat tacttatctg ggcttgatct gaccagtga atgacattgc cctatttggg 180  
 cctctgaggt tctatttagc tttgcagatg tacatagtat cccagtgatc tgcaaaatta 240  
 atgccttttc caagaaaaaa tcttttcttc tctgtatcag ttaattctga cagtgttagt 300  
 gattctgtct tcattatagg ccttatttcc attatctctt tctttatagt attttttggt 360  
 ataaagaaaa cagtctttct gtgtatacct acggatgagg gtattattta aactgccaac 420  
 aatatccaag acatggtcaa t 441

<210> 51  
 <211> 393  
 <212> DNA  
 <213> homo sapiens

<400> 51  
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 taattaggtt attgaccatg tcttgatat tgttggcagt ttaaataata ccctcatccg 120  
 taggtatata cagaaagact gttttcttta taacaaaaaa tactataaag aaagagataa 180  
 tggaaataag gcctataatg aagacagaat cactaacact gtcagaatta actgatacag 240  
 agaagaaaaag attttttctt ggaaaaggca ttaattttgc agatcactgg gatactatgt 300  
 acatctgcaa agctaaatag aacctcagag gtccaaatag ggcaatgtca tttcactggt 360  
 cagatcaagc ccagataagt aatcacagaa aac 393

<210> 52  
 <211> 427  
 <212> DNA  
 <213> homo sapiens

<400> 52  
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 cttttgaatc tagaaaacaa gagaaatgca aagtcattat tccctcattc tatgcttcca 120

2486-109REPLACEMENTSEQLISTCOPY2.TXT

tttactctaa	gaattcagaa	acaaacatgt	gggtaacttc	ctgttatctt	aaaaaaagaa	180
tcaccccttc	ggattccct	taactatctg	gaacttgtag	tgctatttta	taattttacca	240
tgtgacataa	ttgtttgacc	tgcctctttt	atttgatgca	tgacttctca	gagaacctgt	300
tatcaactca	ctgtgtaaaa	ccacgatgaa	atgaaggata	actgatcaca	aagaattatg	360
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atatacct						427

<210> 53  
 <211> 417  
 <212> DNA  
 <213> homo sapiens

<400> 53						
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ttcctttttct	tgtctatcag	tcaccttgaa	actggtaatc	tgattcaagt	taaacaatgt	180
tccttttgaa	tctagaaaac	aagagaaaatg	caaagtcatt	attccctcat	tctatgcttc	240
catttactct	aagaattcag	aaacaaacat	gtgggtaact	tcctgttatc	ttaaaaaaag	300
aatcatccct	tcggtattcc	cttaactatc	tggaacttgt	actgtcattt	tataatttac	360
catgtgacat	aattgtttga	cctgcctctt	ttatttgatg	catgacttct	cagagaa	417

<210> 54  
 <211> 362  
 <212> DNA  
 <213> homo sapiens

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gcaaagtcac	tattccctca	ttctatgctt	ccatttactc	taagaattca	gaaacaaaca	180
tgtgggtaac	ttcctgttat	cttaaaaaaa	gaatcatccc	ttcgggtattc	ccttaactat	240
ctggaacttg	tactgtcatt	ttataattta	ccatgtgaca	taattgtttg	acctgcctct	300
tttatttgat	gcatgacttc	tcagagaacc	tgttatcaac	tcactgtgta	aaaccacgat	360
ga						362

<210> 55  
 <211> 236  
 <212> DNA  
 <213> homo sapiens

<400> 55						
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gaaatgcaaa	gtcattattc	cctcattcta	tgcttccatt	tactctaaga	attcagaaac	180
aaacatgtgg	gtaacttcct	gttatcttaa	aaaaagaatc	atcccttcgg	tcgacg	236

<210> 56  
 <211> 368  
 <212> DNA  
 <213> homo sapiens

<400> 56						
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agaaatgtct	gctttacctgt	agacttttaaa	aacaaacaaa	aaaaacaaac	aaaatttttg	180
gagcatttta	tcattttttt	tctcctttta	tctcctttgt	aatctttattg	tctcctgagt	240
aaatatacac	ataaatgttt	ggggattcat	tgctgctaga	ttatatcagg	tgtttacata	300
gtgtctacta	tatgtctgtg	ataagctttt	tcctaaaaat	agttatcctc	ttttgtagtg	360
tttttccc						368

<210> 57  
 <211> 153  
 <212> DNA

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

&lt;213&gt; homo sapiens

&lt;400&gt; 57

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cttttgaatc	tagaaaacaa	gagaaatgca	aagtcattat	tccctcattc	tatgcttcca	120
tttactctaa	gaattcagaa	acaaacatgt	ggg			153

&lt;210&gt; 58

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 58

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tagaaatgtc	tgcttactgt	agacttttaa	aacaaacaaa	aaaacaaaca	aatthttgga	180
gcatttaatc	attthttttc	tcctttttatc	tcctthtgta	atcttattgt	ctcctgagta	240
aatatacaca	taaattsttk	gggattcatt	gctgbhagat	tatatcaggt	gtttacatag	300
tgtctactat	atgctgttga	taag				324

&lt;210&gt; 59

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 59

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agaattcaga	aacaaacatg	tgggtaactt	cctgtttatct	taaaaaaaga	atcatccctt	180
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actgtgtaaa	accacgatga	aatgaaggat	aactgatcac	aaagaattat	gtcttttgag	360
atccaacaaa	tttacaaatt	ataagagaaa	aatgcaattt	tttaaaaaag	gatatc	416

&lt;210&gt; 60

&lt;211&gt; 2489

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 60

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gttgggtcca	ggaagacatg	ctgactttgc	tggaatgcat	gaagaacaac	cttccatcca	300
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aagacttttc	tggagacatg	tgcaagctca	aatgggtgga	gattttcta	gaggtgagga	420
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aagggggcaa	ggggcgctcc	gagaagccca	agcggcccg	gtcggccatg	ttcatcttct	1320
cggaggagaa	acggcggcag	ctgcaggagg	agcggcctga	gctctccgag	agcgagctga	1380

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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cccgagaggc ggcgctcaag gctcagtcgg agaggaagcc cggcggggag cgcgaggaac 1500
ggggcaagct gcccgagtcg cccaaaagag ctgaggagat ctggcaacag agcgttatcg 1560
gcgactacct ggcccgcctc aagaatgacc ggggtgaaggc cttgaaagcc atggaaatga 1620
cctggaataa catggaaaag aaggagaaac tgatgtggat taagaaggca gccgaagacc 1680
aaaagcgata tgagagagag ctgagtgaga tgcgggcacc tccagctgct acaaattctt 1740
ccaagaagat gaaattccag ggagaaccca agaagcctcc catgaacggt taccagaagt 1800
tctcccagga gctgctgtcc aatggggagc tgaaccacct gccgctgaag gagcgcattg 1860
tggagatcgg cagtcgctgg cagcgcattc cccagagcca gaaggagcac tacaaaaagc 1920
tggccgagga gcagcaaaag cagtacaagg tgcacctgga cctctgggtt aagagcctgt 1980
ctccccagga ccgtgcagca tataaagagt acatctccaa taaacgtaag agcatgacca 2040
agctgcgagg cccaaacccc aaatccagcc ggactactct gcagtccaag tcggagtccg 2100
aggaggatga tgaagaggat gaggatgacg aggacgagga tgaagaagag gaagatgatg 2160
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gcgaggatgg ggatgagaat gaagaggatg acgaggacga agacgacgac gaggatgacg 2280
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ctggcctccc ccactttctt tctttcttt 2489

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&lt;210&gt; 61

&lt;211&gt; 727

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 61

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Lys Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
20      25      30
Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr
35      40      45
Thr Glu Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser
50      55      60
Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
65      70      75      80
Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val
85      90      95
Lys Asn Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro
100     105     110
Lys Lys Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala
115     120     125
Lys Tyr Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys
130     135     140
Ile Leu Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys
145     150     155     160
Tyr Ile Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu
165     170     175
Ala Arg Phe Arg Glu Asp His Pro Asp Leu Ile Gln Asn Ala Lys Lys
180     185     190
Ser Asp Ile Pro Glu Lys Pro Lys Thr Pro Gln Gln Leu Trp Tyr Thr
195     200     205
His Glu Lys Lys Val Tyr Leu Lys Val Arg Pro Asp Glu Ile Met Arg
210     215     220
Asp Tyr Ile Gln Lys His Pro Glu Leu Asn Ile Ser Glu Glu Gly Ile
225     230     235     240
Thr Lys Ser Thr Leu Thr Lys Ala Glu Arg Gln Leu Lys Asp Lys Phe
245     250     255
Asp Gly Arg Pro Thr Lys Pro Pro Asn Ser Tyr Ser Leu Tyr Cys
260     265     270
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275     280     285
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<213> homo sapiens
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 <223> n = A,T,C or G

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 taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag 180  
 aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg 240  
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 agatgaagat gtgccttcct ctgagtgggtg aaatccagat gtagtcagtg gttttctttc 360  
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 tncatca 607

<210> 63  
 <211> 402  
 <212> DNA  
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 aatttgagtg tgatcttagt tgttgtgtgg tgtatttgac tgggtggaat tattggagag 240  
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 tacctgagtt tcatacataa agctctgtac atttaaaagg tt 402

<210> 64  
 <211> 607  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> 602  
 <223> n = A,T,C or G

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 taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag 180  
 aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg 240  
 atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc 300  
 agatgaagat gtgccttcct ctgagtgggtg aaatccagat gtagtcagtg gttttctttc 360  
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 atgctttcag tagccggacc tctgtagctt ttgtgttcga atgggtggcgt ctaagtgttc 540  
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<210> 65  
 <211> 317  
 <212> DNA  
 <213> homo sapiens

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 17, 25, 37, 41, 53, 68, 70, 144

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 65

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ggaaaaaatg	actgtga					317

&lt;210&gt; 66

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 66

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gagaagttaa	ccattcagct	tcagttgtcc	caaaaatctt	cagaatcaga	attatccaaa	180
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&lt;212&gt; DNA

&lt;213&gt; homo sapiens

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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 Glu Ser Glu Gln Gln Tyr Phe Glu Ile Glu Lys Arg Leu Ser His Ser  
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 Gln Glu Arg Leu Val Asn Glu Thr Arg Glu Cys Gln Ser Leu Arg Leu  
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 Glu Leu Glu Lys Leu Asn Asn Gln Leu Lys Ala Leu Thr Glu Lys Asn  
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 Lys Glu Leu Glu Ile Ala Gln Asp Arg Asn Ile Ala Ile Gln Ser Gln  
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 Phe Thr Arg Thr Lys Glu Glu Leu Glu Ala Glu Lys Arg Asp Leu Ile  
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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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Asn	Gly	Leu	Lys	Thr	Ser	Asn	Glu	His	Leu	Gln	Lys	His	Val	Glu	Asp
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Leu	Leu	Thr	Lys	Leu	Lys	Glu	Ala	Lys	Glu	Gln	Gln	Ala	Ser	Met	Glu
			260					265					270		
Glu	Lys	Phe	His	Asn	Glu	Leu	Asn	Ala	His	Ile	Lys	Leu	Ser	Asn	Leu
		275					280					285			
Tyr	Lys	Ser	Ala	Ala	Asp	Asp	Ser	Glu	Ala	Lys	Ser	Asn	Glu	Leu	Thr
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Arg	Ala	Val	Glu	Glu	Leu	His	Lys	Leu	Leu	Lys	Glu	Ala	Gly	Glu	Ala
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Asn	Lys	Ala	Ile	Gln	Asp	His	Leu	Leu	Glu	Val	Glu	Gln	Ser	Lys	Asp
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Lys	Ala	Pro	Ile	Leu	Lys	Arg	Gln	Arg	Glu	Glu	Tyr	Glu	Arg	Ala	Gln
		435					440					445			
Lys	Ala	Val	Ala	Ser	Leu	Ser	Val	Lys	Leu	Glu	Gln	Ala	Met	Lys	Glu
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Val	Leu	Glu	Arg	Asp	Asn	Arg	Arg	Met	Glu	Ile	Gln	Val	Lys	Asp	Leu
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Asn	His	Val	Ile	Arg	Asp	Glu	Glu	Val	Ser	Ser	Ala	Asp	Ile	Ser	Ser
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Gly	Glu	Thr	Arg	Glu	Arg	Glu	Glu	Gln	Glu	Thr	Thr	Ser	Ser	Lys	Ile
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Thr	Pro	Lys	Arg	Pro	Ser	Thr	Ser	Gln	Thr	Val	Ser	Thr	Pro	Ala	Pro
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## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

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Ser	Asn	930	Lys	Glu	Asp	Val	Asp	935	Asp	Leu	Val	Ser	Gln	940	Leu	Arg	Gln	Thr
Glu	Glu	945	Gln	Val	Asn	Asp	Leu	950	Lys	Glu	Arg	Leu	Lys	955	Thr	Ser	Thr	Ser
Asn	Val	965	Glu	Gln	Tyr	Gln	Ala	970	Met	Val	Thr	Ser	Leu	975	Glu	Glu	Ser	Leu
Asn	Lys	980	Glu	Lys	Gln	Val	Thr	985	Glu	Glu	Val	Arg	Lys	990	Asn	Ile	Glu	Val
Arg	Leu	995	Glu	Ser	Ala	Glu	Phe	1000	Gln	Thr	Gln	Leu	Glu	1005	Lys	Lys	Leu	Leu
Met	Glu	1010	Val	Glu	Lys	Glu	Lys	1015	Gln	Glu	Leu	Gln	Asp	1020	Asp	Lys	Arg	Arg
Ala	Ile	1025	Glu	Ser	Met	Glu	Gln	1030	Gln	Leu	Ser	Glu	Leu	1035	Lys	Lys	Thr	Leu
Ser	Ser	1045	Val	Gln	Asn	Glu	Val	1050	Gln	Glu	Ala	Leu	Gln	1055	Arg	Ala	Ser	Thr
Ala	Leu	1060	Ser	Asn	Glu	Gln	Gln	1065	Ala	Arg	Arg	Asp	Cys	1070	Gln	Glu	Gln	Ala
Lys	Ile	1075	Ala	Val	Glu	Ala	Gln	1080	Asn	Lys	Tyr	Glu	Arg	1085	Glu	Leu	Met	Leu
His	Ala	1090	Ala	Asp	Val	Glu	Ala	1095	Leu	Gln	Ala	Ala	Lys	1100	Glu	Gln	Val	Ser
Lys	Met	1105	Ala	Ser	Val	Arg	Gln	1110	His	Leu	Glu	Glu	Thr	1115	Thr	Gln	Lys	Ala
Glu	Ser	1125	Gln	Leu	Leu	Glu	Cys	1130	Lys	Ala	Ser	Trp	Glu	1135	Glu	Arg	Glu	Arg
Met	Leu	1140	Lys	Asp	Glu	Val	Ser	1145	Lys	Cys	Val	Cys	Arg	1150	Cys	Glu	Asp	Leu
Glu	Lys	1155	Gln	Asn	Arg	Leu	Leu	1160	His	Asp	Gln	Ile	Glu	1165	Lys	Leu	Ser	Asp

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

Lys Val Val Ala Ser Val Lys Glu Gly Val Gln Gly Pro Leu Asn Val  
 1170 1175 1180  
 Ser Leu Ser Glu Glu Gly Lys Ser Gln Glu Gln Ile Leu Glu Ile Leu  
 1185 1190 1195 1200  
 Arg Phe Ile Arg Arg Glu Lys Glu Ile Ala Glu Thr Arg Phe Glu Val  
 1205 1210 1215  
 Ala Gln Val Glu Ser Leu Arg Tyr Arg Gln Arg Val Glu Leu Leu Glu  
 1220 1225 1230  
 Arg Glu Leu Gln Glu Leu Glu Asp Ser Leu Asn Ala Glu Arg Glu Lys  
 1235 1240 1245  
 Val Gln Val Thr Ala Lys Thr Met Ala Gln His Glu Glu Leu Met Lys  
 1250 1255 1260  
 Lys Thr Glu Thr Met Asn Val Val Met Glu Thr Asn Lys Met Leu Arg  
 1265 1270 1275 1280  
 Glu Glu Lys Glu Arg Leu Glu Gln Asp Leu Gln Gln Met Gln Ala Lys  
 1285 1290 1295  
 Val Arg Lys Leu Glu Leu Asp Ile Leu Pro Leu Gln Glu Ala Asn Ala  
 1300 1305 1310  
 Glu Leu Ser Glu Lys Ser Gly Met Leu Gln Ala Glu Lys Lys Leu Leu  
 1315 1320 1325  
 Glu Glu Asp Val Lys Arg Trp Lys Ala Arg Asn Gln His Leu Val Ser  
 1330 1335 1340  
 Gln Gln Lys Asp Pro Asp Thr Glu Glu Tyr Arg Lys Leu Leu Ser Glu  
 1345 1350 1355 1360  
 Lys Glu Val His Thr Lys Arg Ile Gln Gln Leu Thr Glu Glu Ile Gly  
 1365 1370 1375  
 Arg Leu Lys Ala Glu Ile Ala Arg Ser Asn Ala Ser Leu Thr Asn Asn  
 1380 1385 1390  
 Gln Asn Leu Ile Gln Ser Leu Lys Glu Asp Leu Asn Lys Val Arg Thr  
 1395 1400 1405  
 Glu Lys Glu Thr Ile Gln Lys Asp Leu Asp Ala Lys Ile Ile Asp Ile  
 1410 1415 1420  
 Gln Glu Lys Val Lys Thr Ile Thr Gln Val Lys Lys Ile Gly Arg Arg  
 1425 1430 1435 1440  
 Tyr Lys Thr Gln Tyr Glu Glu Leu Lys Ala Gln Gln Asp Lys Val Met  
 1445 1450 1455  
 Glu Thr Ser Ala Gln Ser Ser Gly Asp His Gln Glu Gln His Val Ser  
 1460 1465 1470  
 Val Gln Glu Met Gln Glu Leu Lys Glu Thr Leu Asn Gln Ala Glu Thr  
 1475 1480 1485  
 Lys Ser Lys Ser Leu Glu Ser Gln Val Glu Asn Leu Gln Lys Thr Leu  
 1490 1495 1500  
 Ser Glu Lys Glu Thr Glu Ala Arg Asn Leu Gln Glu Gln Thr Val Gln  
 1505 1510 1515 1520  
 Leu Gln Ser Glu Leu Ser Arg Leu Arg Gln Asp Leu Gln Asp Arg Thr  
 1525 1530 1535  
 Thr Gln Glu Glu Gln Leu Arg Gln Gln Ile Thr Glu Lys Glu Glu Lys  
 1540 1545 1550  
 Thr Arg Lys Ala Ile Val Ala Ala Lys Ser Lys Ile Ala His Leu Ala  
 1555 1560 1565  
 Gly Val Lys Asp Gln Leu Thr Lys Glu Asn Glu Glu Leu Lys Gln Arg  
 1570 1575 1580  
 Asn Gly Ala Leu Asp Gln Gln Lys Asp Glu Leu Asp Val Arg Ile Thr  
 1585 1590 1595 1600  
 Ala Leu Lys Ser Gln Tyr Glu Gly Arg Ile Ser Arg Leu Glu Arg Glu  
 1605 1610 1615  
 Leu Arg Glu His Gln Glu Arg His Leu Glu Gln Arg Asp Glu Pro Gln  
 1620 1625 1630  
 Glu Pro Ser Asn Lys Val Pro Glu Gln Gln Arg Gln Ile Thr Leu Lys  
 1635 1640 1645  
 Thr Thr Pro Ala Ser Gly Glu Arg Gly Ile Ala Ser Thr Ser Asp Pro  
 1650 1655 1660  
 Pro Thr Ala Asn Ile Lys Pro Thr Pro Val Val Ser Thr Pro Ser Lys

## 2486-109REPLACEMENTSEQLISTCOPY2.TXT

1665 1670 1675 1680  
 Val Thr Ala Ala Ala Met Ala Gly Asn Lys Ser Thr Pro Arg Ala Ser  
 1685 1690 1695  
 Ile Arg Pro Met Val Thr Pro Ala Thr Val Thr Asn Pro Thr Thr Thr  
 1700 1705 1710  
 Pro Thr Ala Thr Val Met Pro Thr Thr Gln Val Glu Ser Gln Glu Ala  
 1715 1720 1725  
 Met Gln Ser Glu Gly Pro Val Glu His Val Pro Val Phe Gly Ser Thr  
 1730 1735 1740  
 Ser Gly Ser Val Arg Ser Thr Ser Pro Asn Val Gln Pro Ser Ile Ser  
 1745 1750 1755 1760  
 Gln Pro Ile Leu Thr Val Gln Gln Gln Thr Gln Ala Thr Ala Phe Val  
 1765 1770 1775  
 Gln Pro Thr Gln Gln Ser His Pro Gln Ile Glu Pro Ala Asn Gln Glu  
 1780 1785 1790  
 Leu Ser Ser Asn Ile Val Glu Val Val Gln Ser Ser Pro Val Glu Arg  
 1795 1800 1805  
 Pro Ser Thr Ser Thr Ala Val Phe Gly Thr Val Ser Ala Thr Pro Ser  
 1810 1815 1820  
 Ser Ser Leu Pro Lys Arg Thr Arg Glu Glu Glu Asp Ser Thr Ile  
 1825 1830 1835 1840  
 Glu Ala Ser Asp Gln Val Ser Asp Asp Thr Val Glu Met Pro Leu Pro  
 1845 1850 1855  
 Lys Lys Leu Lys Ser Val Thr Pro Val Gly Thr Glu Glu Glu Val Met  
 1860 1865 1870  
 Ala Glu Glu Ser Thr Asp Gly Glu Val Glu Thr Gln Val Tyr Asn Gln  
 1875 1880 1885  
 Asp Ser Gln Asp Ser Ile Gly Glu Gly Val Thr Gln Gly Asp Tyr Thr  
 1890 1895 1900  
 Pro Met Glu Asp Ser Glu Glu Thr Ser Gln Ser Leu Gln Ile Asp Leu  
 1905 1910 1915 1920  
 Gly Pro Leu Gln Ser Asp Gln Gln Thr Thr Thr Ser Ser Gln Asp Gly  
 1925 1930 1935  
 Gln Gly Lys Gly Asp Asp Val Ile Val Ile Asp Ser Asp Asp Glu Glu  
 1940 1945 1950  
 Glu Asp Glu Glu Asp Asp Asp Asp Asp Glu Asp Asp Thr Gly Met Gly  
 1955 1960 1965  
 Asp Glu Gly Glu Asp Ser Asn Glu Gly Thr Gly Ser Ala Asp Gly Asn  
 1970 1975 1980  
 Asp Gly Tyr Glu Ala Asp Asp Ala Glu Gly Gly Asp Gly Thr Asp Pro  
 1985 1990 1995 2000  
 Gly Thr Glu Thr Glu Glu Ser Met Gly Gly Gly Glu Gly Asn His Arg  
 2005 2010 2015  
 Ala Ala Asp Ser Gln Asn Ser Gly Glu Gly Asn Thr Gly Ala Ala Glu  
 2020 2025 2030  
 Ser Ser Phe Ser Gln Glu Val Ser Arg Glu Gln Gln Pro Ser Ser Ala  
 2035 2040 2045  
 Ser Glu Arg Gln Ala Pro Arg Ala Pro Gln Ser Pro Arg Arg Pro Pro  
 2050 2055 2060  
 His Pro Leu Pro Pro Arg Leu Thr Ile His Ala Pro Pro Gln Glu Leu  
 2065 2070 2075 2080  
 Gly Pro Pro Val Gln Arg Ile Gln Met Thr Arg Arg Gln Ser Val Gly  
 2085 2090 2095  
 Arg Gly Leu Gln Leu Thr Pro Gly Ile Gly Gly Met Gln Gln His Phe  
 2100 2105 2110  
 Phe Asp Asp Glu Asp Arg Thr Val Pro Ser Thr Pro Thr Leu Val Val  
 2115 2120 2125  
 Pro His Arg Thr Asp Gly Phe Ala Glu Ala Ile His Ser Pro Gln Val  
 2130 2135 2140  
 Ala Gly Val Pro Arg Phe Arg Phe Gly Pro Pro Glu Asp Met Pro Gln  
 2145 2150 2155 2160  
 Thr Ser Ser Ser His Ser Asp Leu Gly Gln Leu Ala Ser Gln Gly Gly  
 2165 2170 2175

2486-109REPLACEMENTSEQLISTCOPY2.TXT

Leu Gly Met Tyr Glu Thr Pro Leu Phe Leu Ala His Glu Glu Glu Ser  
 2180 2185 2190  
 Gly Gly Arg Ser Val Pro Thr Thr Pro Leu Gln Val Ala Ala Pro Val  
 2195 2200 2205  
 Thr Val Phe Thr Glu Ser Thr Thr Ser Asp Ala Ser Glu His Ala Ser  
 2210 2215 2220  
 Gln Ser Val Pro Met Val Thr Thr Ser Thr Gly Thr Leu Ser Thr Thr  
 2225 2230 2235 2240  
 Asn Glu Thr Ala Thr Gly Asp Asp Gly Asp Glu Val Phe Val Glu Ala  
 2245 2250 2255  
 Glu Ser Glu Gly Ile Ser Ser Glu Ala Gly Leu Glu Ile Asp Ser Gln  
 2260 2265 2270  
 Gln Glu Glu Glu Pro Val Gln Ala Ser Asp Glu Ser Asp Leu Pro Ser  
 2275 2280 2285  
 Thr Ser Gln Asp Pro Pro Ser Ser Ser Val Asp Thr Ser Ser Ser  
 2290 2295 2300  
 Gln Pro Lys Pro Phe Arg Arg Val Arg Leu Gln Thr Thr Leu Arg Gln  
 2305 2310 2315 2320  
 Gly Val Arg Gly Arg Gln Phe Asn Arg Gln Arg Gly Val Ser His Ala  
 2325 2330 2335  
 Met Gly Gly Arg Gly Gly Ile Asn Arg Gly Asn Ile Asn  
 2340 2345

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Applicant: Dranoff, et al.

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Docket: 2486/109

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Filing Date: 1999-08-06

OS: Windows 5.01

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Copy 1 of 2